

RAW SEQUENCE LISTING

DATE: 02/24/2003

PATENT APPLICATION: US/09/690,885

TIME: 08:10:04

Input Set : A:\1422-319 Parent SL.txt
Output Set: N:\CRF4\02242003\1690885.raw

## SEQUENCE LISTING

```
4 (1) GENERAL INFORMATION:
              (i) APPLICATE: SAGAWA, HIROAKI
                              UENO, HARIMI
                              OUHIMA, ATRUSHI
                             FARO, IRUNOSHIN
            (ii) TITLE OF INVENTION: PLASMID
     1:
     13
           (iii) NUMEER + F SEQUENCES: 13
     1 :
            (iv) CORESTEANCE ADDRESS:
     16
                   (A) ACCHESCHE: FIRCH, STEWART, KOLASCH & BIRCH, LLP
                   (E) CIEEET: PO BOX 747
     1 :
                   FOR MITY: FALLS CHIECE
     1 :-
                   GO JIATE: WA
     1 1
                                                                    ENTERED
                   (E) (COUNTRY: USA
     20
                   (F) CII: Not 49-1047
     . . .
             (v) COMBUTER READABLE FORM:
                   (A) MEDIUM TUPE: Floppy disk
                   (F) 'OMP'TER: 1EM PC compatible
                   (C) OPERATIONS SYSTEM: PC-DOS/MS-DOS
     1: 1
                   (to COSTWARE: Patentin Release #1.0, Version #1.30
             (vi) CURRENT AFPLICATION DATA:
C--> 30
                   (A) APPLICATION NUMBER: US/09/690,885
C--> 31
                   (B) FILING DATE: 18-Oct-2000
                   CONCLASSIFICATION:
     30
          (viii) ATTORNET, AGENT INFORMATION:
     . 1 - 4
     36
                   (A) MAME: WEINER, MARC S.
     , ST
                   F) REGISTRATION NUMBER: 32,181
                   HOT REPERENCE DOCKET NUMBER: 1422-0319P
     5.4
             (ix) THE ECOMMUTE CATION INFORMATION:
     300
                   PAN METAPI HOUR: MODEL 05-8000
     ·; :
                   (F) TELEPRE: 10:-101-8050
     44 (2) INFORMATION FOR SEQ 11 NO: 1:
     4.4
             (i) SECUENCE CHARACTERISTICS:
     47
                   (A) IEMGTH: Lot armic acids
     40
                   (F) TYFE: amino actio
     ., G
                   (C) CIFABLEDNESS: single
     1.11
                   (1) TOPOLOGY: linear
            (ii) MOLECULE TYPE: protein
     \mathbf{L}_{1} \mathbf{U}_{2}
            (ix) FEATURE:
                   (A) NAME, FEY: Modif.ed-site
     5+,
     57
                   (i) I CCATION: 2
                   (b) OTHER INFORMATION: /note= "2=Val or Leu"
     61
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
```

# RAW SEQUENCE LISTING

DATE: 021/24/2003 PATENT APPLICATION: US/09/690,885 TIME: 03:10:04

Input Set : A:\1422-319 Parent SL.txt Output Set: N:\CRF4\02242003\1690885.raw

```
Met Xaa Pro Leu Asp Lys Asp Leu Gln Lys Ala Lys Ile Ser Ile Thr
W --> 63
                                       10
          1 5
          Asp Phe Fhe Glu lle Thr Ash Arg Val Leu Asp Tyr Phe Fro Ash Val
    64
    66
                                     25
           lle Asn Asr. Thr Val Glu Lys Gly Asp Tyr Leu Il€ Ser Ser Ser Asn
    67
    69
                     40
           Ile Ala Gly Tmr Ile Lys The Leu Arg Fro Ile Asm Arg Lys Leu Pne
    70
    7.2
                    5.5
           Ile Gln Glo Lys Lys Val Phe Asn Asp Typ Fhe Gln Lys Leu Ile Ile
    7:
    75
                                            75
                           7.0
           Val Phe Glo Ash Ilo Arg Ash Lys Lys Thr Val Thr Glo Glo Asr Lys
    7 E
    75
                       35
           The Ilo Ilo As; Arg Val Ile Tyr Thr Ile Gln Sln Ser Ile Gly Ile
    74
    8.
                                    105
                    100
           Gly Leu Asp Len Met Val Ash Gin Ash Ser Ala Arg Lys His Val Gly
    83
            130
    8.4
           Asn Ary Pho Glu Glu Leu Ile Ary Val Ile Phe Thr Glu Ile Ser Val
    8.5
           130 135
    € 7
           Ser Ash by: And Thr Val Leu Gin Ile Fro Tyr Glu The Asp Glu Gly
     8- -
                                           155
     9 C.
                     150
           Gln Lys The Tyr Lys Cys Glu Ash Asp lea The The Ser Pro Phe Glu
     1 1
                             170
     1,4 D
           Asn Val Glo. Fer The Asn Lys His Leu Asp Glu Asn Glu Ile Val Val
                       1 + 5.
     114
                            185
     144
           Ser Ile Lys Thr Thr Ser Lys Arp Arg Met Gly Lys Met Phe Ile Asp
                     160
     97
                                100 205
     . 4 4
            Lys lie led beu thu Arg Pne Val Lys His Pro Gln Lys Val Ile Gly
                  医磷黄
     100
                               220
     1:72
             . 10
            The Ene Leu Ash Asp Val Gln Arg Tys Glu Asp Ash Ash The Ser Ehe
     102
                                   235
     100
                            230
            Thr led Val Der Gly bed The Met Val Tyr Thr Lys The Leu Tor Thr
     1.66
                                250 258
     100
            Leu Gla Gly Tie Tyr Tyr Leu Asp Pro Pro Pro Ash Ala Leu Lys Leu
                          245
     134
                ..60 270
     111
             Fro Tyr Cer Ash His Met Lys Arg Phe Ser Asp Leu Ile Thr Glu Asp
     11.
     114
                   -: r
                       28:)
     115
             Leu Glo Lys Leu Ebe Ser Ser
     1: /
             ĨēC
     110
     170 (2) IMPOFMATION FOR SEQ ID NO: 3:
            (i) SEQUENCE CHARACTERICTICS:
                 (A) LENGTH: 885 base pairs
                 (B) THE: nucleic anid
      1. :
                 (C) STRANDELNESS: jouble
      1.5
                 (D: ToFOLOGY: Tanear
      1. 6
            (ii) MOLECULE TYPE: DNA (genomic)
            (xi) SEQUENCE DESCRIPTION: ('EQ ID MO: 2:
      1.5 ATGSTACCAC TOBATAAAGA TTTACAAAAA GCAAAGATTT CAATTACTGA TTTTTTTGAA
                                                                   60
      1 \cdot 3
                                                                   120
      1-7 ATTACAAATA GASTTUTASA TOATTTOCCO AATGTAATCA ATAATACAGT TGAAAAAGGA
      139 GATTATTTAA TATCOTCATO AAATATTGCT GGAACAATAA AATTCOTAAG AOCAATCAAT
                                                                   180
```

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Input Set : A:\1422-319 Parent SL.txt Output Set: N:\CRF4\02242003\1690885.raw

1 1 1	AGAAAGTTAT TIATTCAGGA AAAAAAAGTT TTCAATGATT ATTTTCAAAA ACTGATTAT	A 240
143	B GTTTTTGAAA ATATAAGGAA CAAAAAAACT GTAACAGAGG AAGATAAAAT TATTATTGA	T 300
	CAGGGTAATTT ACACAATAGA GCAATGTATT GGAATTOGIT TAGATTTAAT GGTTAATCA	
	AATAGTGCTA GAAAGGAGG TUGTWAGGA TIIGAAGAAI TAATTAGAGT CATITTAG	
	GAAATATUAG TATOGAATAA AAGAACTIGTA FIACAAATTO CATATGAAAC TGATGAAGG	
	CAGAAAATTI AGAAATGIGA GAATGACOFO AFFATTIOFO OTTTTGAAAA TGTAGAATO	
1	CACAAA CAAA CATO CAHA COAHA COAHATOAHATT GTI GTITTTTAA ITAAAGA CAACIA FCAAAAGA	T EDI
1.600	- ASSATOGGAA AAATUTTTAT AGATAAAATT ITACTTGAAA GGTTTGTTAA ACACCCTCA	Α έδθ
16%	AAAGTTATAG GGATTTTOOT MAATGATGTA CAAAGAAAAG AAGACAACAA TATCAGCTT	T 7.10
1: +	CADACTOSTOT CAS BATTATO TATGOTOTAT ACEAAATOT FAACTACICE TGAASGGAT	C 780
1 · :	TATIATING ATOM MANO MANTOWITS ANACTACCAT AIISTANTCA TATGANANG	A 140
1.15	POTICAGATT TAATTWOMGA AGWOOTINGAA AAAITTAIITOT OOLOT	335
	(2) INFORMATION FOR SEQ ID NO: 3:	
1	i) SEQUENCE CHARACTERISTICS:	
$1 e \approx$	(A) DENGGE: 215 page pairs	
1+1+	E) TYPE: nubleit spid	
170	E) TYPE: nucleit abid C) STEAMDEDMESS: single (D) TOPOSOSY: linear	
1 / 1	(D) TOPOLOGY: linear	
1	(Li) MODECULE TYPE: other nucleic acid	
1	A) DENCERPICON: Guest = "synthetic ONA"	
170	(xi) SEQUENCE DESCRIPTION: SEQ 10 NO: 3:	
1	TARGUARATS TRUNTADAGA GUART WAGO DAGAWAGATO PITGGTTOTG AAFOODAAC	C 60
	ACTEGOCTTA TECHNOLOGY COCCUATOAC CLACCATOCC TAATGACCTE CAGGCATEC.	
1: :.	AGOITHCAIG CCIDCAGGTC ALIANGTACH GCAGGTGTGC TOGAGGGGAA GGAGTGCCT	G 130
1 -	CATGO FITTO ICCUTORCET INTENTIONS GGACA	215
1 😘	( (2) INFORMATION FOR SEL 10 NO: 4:	
1 111	(i) SEQUENCE CHARACTERISTICS:	
1 4%	(A) LEMOTH: .11 base pairs	
1 44	(E) TYPE: nerleid adia (C) THANDEDUEDS: kingle () TOPOIOGY: linear	
1 🖖	I) 10P0100Y: linear	
1 🗥	(ii: MOLECTUR TYPE: other modleic acid	
1'48:		
	(Mi) BEQUENCE LESCHIPTION: SEQ ID NO: 4:	
1111	TATGTCCCAG AGGAWAAWAG CCAAGGAGAA ACGCATGCAG GCACTCCTTC GCCTCGAGC	A 60
110	CACCTGCCGT ACCTAATCAC CTGCAG+CAT GCAAGCTTGC ATGCCTGCAG GTCATTAGG	G 120
	ATGGTAGGIG ATGCGCGCT CCTGCCATAA GGCCACTGGT TGCGATTCAC AACCAAAGA	
.: 2 2	CTATCTGCCT ACATOCOTGT CTATGAACAT ATCCA	215
	(2) INFORMATION FOR SEQ II NO: 5:	
	i - BEQUENTE CHAFACTERITICS:	
. 16	(A) LEDGTH: 18 base pairs	
. 17	,	
. 18	· · · · · · · · · · · · · · · · · · ·	
9		
. : 1		
112		
::7		
::: 9	AGATCTAGAG CAAACAAAAA AACCACUG	28
1 د 2	(2) INFORMATION FOR SEQ ID NO: 6:	

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Input Set : A:\1422-319 Parent SL.txt Our put Set: N:\CRF4\02242003\1690885.raw

```
233
                   (i) SEQUENCE CHARACTERICTICS:
   4.7
                              (A) LENGTH: ...4 base pairs
                              (B) TYPE: n: Leic woid
                                C) OTPANDEDNESS: single
200
                               (D) TOPOLOGY: linear
1. 3.7
                 (+i) MOLECULE TYPE: otro: nucleic acid
                                A) DEMORIPTION: sesc = "synthetic DNA"
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
. 4 / GGTCTAGATO OCA MOGNAJA JAVAG
                                                                                                                                                                     24
.40 (2) INFORMATION FOR SEP 10 Not 7:
                  (i) SEPTEMBE THARATTERS:
. .
                              (A) LENGTH: 100 base pairs
                               SEC TYPE: nucleic soid
. : ;
                               .To :TFANDEMBERS: single
. ., .
                              (So TOPOBOGY: .ir.ar
                 (.i) MOLECULE TYPE: other nucleic acid
: : .
                              TAR DELICETEDA: Gest = "synthetic DNA"
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
. CONTROL OF CONTROL OF A CONTR
                                                                                                                                                                     60
, \kappa = \text{CACAGGARA} \in \text{AGACTMATTOG} = \text{CTAAGTMACT} = \text{AGTGAATTOG}
                                                                                                                                                                   100
 * * (2) INFORMATION FOR SECTIONS: 8:
                  (i) JENJENCH CHARACTERICTICS:
'As LEMETH: 15" pare pairs
                               (B) TYPE: number acid
                               OCT :TEATHERNESS: single
. 14
- . .
                              (CD) TOROLOWY: linear
                 (Li, MODECTLE TYPE: other nucleic acid
                              A) DENTE PTION: /desc = "synthetic DNA"
. 9 -
                 (xi: SEQUENCE DESCRIPTION: SEQ ID NO: 8:
. - CGAATTCACT AGITACTIAN + MAIPPICT GTTTCCIGIG AAGCTTGGAA TTGTTATCCG
                                                                                                                                                                     60
INVICTOACAATTO OGIATIOTAT AGTOTOACCI AAATOTOGAG
                                                                                                                                                                   100
. - (2) INFOFMATION FOR SEQ (D D): 9:
                  - i - sequence characteristics:
                              (A) DENGIH: 1. base pairs
. 4.
1.5
                              (P) THE: multic acid
14.4
                              (C) CTHANDELTURES: Jingle
1 15
                              (I) TOROGOGY: linear
. .
                 (Li) MOIECULE TYPE: other nucleic acid
1.49
                              (A) DECCEIFTION: /:esc = "synthetic ENA"
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
F E AATOCCATGG AACGGTACGA ATGTCTG
                                                                                                                                                                     27
BOY (2) INFORMATION FOR SEQ ID NO: 10:
                  (i) SEQUEDOR CHARACTERISTICS:
1.14
:10
                              (A) IEMOTH: U: base pairs
11
                              (B) TYPE: nucleic acid
1:1:
                              (C) CILANDEDNESS: single
1.
                              (D) ".OPOLOGY: linear
31!
              (ii) MCLECULE TYPE: other nucleic acid
516
                              (A) LESCHIPTION: /desc = "synthetic DNA"
```

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Input Set : A:\1422-319 Parent SL.txt
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```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
323 CCGGCCATGG TTATTTTTGA TACCADACT
                                                                              29
30% (2) INFORMATION FOR SECTION 10: 11:
3.: `
        (i) BEDOENCE CHARACTERISIES:
2.18
              (A) LEMPIH: 16 base pairs
5.5 🖅
              HER TYPE: nu leid adid
              (C) STRANDEDUESS: single
5 - 1
              -120 TOPON GY: linear
        (ii) MOLECULE TYPE: other nucleic acid
2.54
              TA) DESCRIPTION: 'desc = "synthetic DNA"
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
5 5 4
SHI TAACTIGAAT COATGGGIIC FCACCI
                                                                              26
14 - (2) INFORMATION FOR SECTIONE: 12:
(i) SEQUENCE CHARACTERISTICS:
5 11
              (A) DEMOTE: . 9 pare pairs
347
              NE/ TYPE: numbered acid
? : :-
              (0) STRAMBEDNESS: single
2.4
              SER TOPOLOGY: linear
        (ii) MOLECULE TYPE: other nucleic acid
              (A) DESCRIPTION: desc = "synthetic DNA"
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
31 * TACTCAGTAG CCATGCCT TT CATAGACCG
                                                                              29
Bel (2) INFORMATION FOR SECTION WG: 13:
24. -
         dit sequence characteristics:
5+4
              (A) LENGTH: 418 amino acids
4.4.
              (P) TYPE: amino a mid
Sec.
              (C) STRAM EDMESS: single
30 1
              (I) TOPOLOGY: linear
314514
        (ii MOLECULE TYPE: peptide
5 .;
        (xi, SEQUENCE DESCRIPTION: SEQ ID NO: 13:
5.24
        Met Ash Glu lie A.a She Asp Ash Tyr Ser Tyr Ile Pro Lys Leu Lys
ç ----
                                               1.0
3/4
         Leu Tyr Ser Glo Lie Glo Leu Lys Pro Phe Phe Ile Ser Lys Asn Gly
5 ...
                                           25
                                                                30
5.-..
         Ser Deu Phe Ast. Val Asp Ala He Asp Phe Leu Arg Lys Leu Glu Ser
3-3
                                       411
5.4
         Ash Ser Val Asp Leu Ile Phe Ala Asp Pro Pro Tyr Ash Ile Lys Lys
324
         4,17
                                  55
                                                       60
         Ala Glu Trp Asp ile Fhe Ser Ser Gln Asr. Glu Tyr Leu Glu Trp Ser
                                                   75
300
                              70
3.41
         Lys Gin Trp II. Met Gl. Ala His Arg Val Leu Lys Asp Asn Gly Ser
3.1.1
                          3.
                                               90
3 44
         Leu Tyr Val Cyk Gly Pho Ser Glu Ile Leu Ala Asp Ile Lys Phe Ile
2-41,
                                                               110
                     100
                                           105
397
         The Ser Lys Tyr Phe Hir Ser Cys Lys Trp Leu Ile Trp Phe Tyr Arg
3.45
                                                           125
                 115
                                      1:0
4+ 6:
         Ash Lys Ala Ash Leu Gly Lys Asp Trp Gly Arg Ser His Glu Ser Ile
41.
                                  135
                                                       140
         Leu Leu Ard Lys Ser Lys Ann Phe Ile Fhe Asn Ile Asp Glu Ala
465
```